



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 120495

TO: Bao-thuy Nguyen
Location: REM-3D51/3C70
Art Unit: 1641
Wednesday, April 28, 2004

Case Serial Number: 09/845729

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

RUSH

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120495

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Tuesday, April 27, 2004 1:58 PM
To: Nguyen, Bao-Thuy; STIC-Biotech/ChemLib
Subject: RE: 09/845,729

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

Fr m: Nguyen, Bao-Thuy
Sent: Tuesday, April 27, 2004 12:44 PM
To: Chan, Christina
Subject: 09/845,729

Chris:

Please approve a rush search for 09/845,729. It is an overdue amendment that was reassigned to me yesterday. Thank You.

STIC-BIOTECH: Please search residues 2-14 of SEQ ID No. 1.

Thank You
Bao-Thuy Nguyen
AU 1641
(571) 272-0824
Remsen 3D51
Mailbox 3C70

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2004, 16:22:48 ; Search time 21 Seconds
(without alignments)
59.547 Million cell updates/sec

Title: US-09-845-729A-1_COPY_2_14

Perfect score: 65

Sequence: 1 SESDFLAEGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	93.8	16	2 H29501	fibrinopeptide A -
2	57	87.7	16	2 C28854	fibrinopeptide A -
3	57	87.7	16	2 A24180	fibrinogen alpha c
4	57	87.7	16	2 B24180	fibrinogen alpha c
5	57	87.7	16	2 A28854	fibrinopeptide A -
6	57	87.7	16	2 B28854	fibrinopeptide A -
7	57	87.7	16	2 A29501	fibrinopeptide A -
8	57	87.7	644	1 FGHUA	fibrinogen alpha c
9	57	87.7	866	2 D4234	fibrinogen alpha c
10	52	80.0	15	2 F29501	fibrinopeptide A -
11	51	78.5	16	2 G29501	fibrinopeptide A -
12	51	78.5	28	2 A05296	fibrinogen alpha c
13	49	75.4	17	2 E29501	fibrinopeptide A -
14	48	73.8	15	2 I29501	fibrinopeptide A -
15	48	73.8	19	2 B29501	fibrinopeptide A -
16	48	73.8	19	2 C29501	fibrinopeptide A -
17	48	73.8	311	2 A05294	fibrinogen alpha c
18	40	61.5	15	2 JP0101	fibrinogen alpha c
19	40	61.5	280	2 H9800	hypothetical prote
20	39	60.0	236	2 S48967	dimethylallyltrans
21	39	60.0	245	2 AG0701	Orf 245 protein [i
22	39	60.0	271	2 S18730	aminoglycoside N3
23	39	60.0	324	2 D70943	hypothetical prote
24	39	60.0	705	2 T31157	hypothetical prote
25	38.5	59.2	732	2 AB2732	conserved hypothet
26	38.5	59.2	741	2 B97513	probable secreted
27	38	58.5	575	2 T48224	probable homeodoma
28	38	58.5	611	1 S12566	translation initia
29	38	58.5	652	2 AD2316	hypothetical prote

30	38	58.5	669	2	A72718	hypothetical prote
31	38	58.5	686	2	T08919	hypothetical prote
32	38	58.5	727	2	T08920	hypothetical prote
33	38	58.5	742	2	T00371	hypothetical prote
34	37	56.9	149	2	G85534	hypothetical prote
35	37	56.9	149	2	C90684	hypothetical prote
36	37	56.9	164	2	E70639	hypothetical prote
37	37	56.9	302	2	F90526	hypothetical prote
38	37	56.9	363	2	G71544	hypothetical prote
39	37	56.9	410	2	F96683	hypothetical prote
40	37	56.9	412	2	S28423	isocitrate dehydro
41	37	56.9	415	2	S65065	isocitrate dehydro
42	37	56.9	416	2	S47013	isocitrate dehydro
43	37	56.9	416	2	A96585	NADP specific isoc
44	37	56.9	421	2	D69643	imidazolone-5-prop
45	37	56.9	433	2	T09619	isocitrate dehydro

ALIGNMENTS

RESULT 1

H29501

fibrinopeptide A - gray seal

C:Species: Halichoerus grypus (gray seal)

C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000

C:Accession: H29501

R:Blombaeck, B.; Blombaeck, M.; Hann, C.

unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser

A:Reference number: A29501

A:Accession: H29501

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <BLO>

C:Superfamily: fibrinogen beta chain; fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic

Query Match 93.8%; Score 61; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13

DB 5 ESDFLAEGGGVR 16

RESULT 2

C28854

fibrinopeptide A - gelada baboon

C:Species: Theropithecus gelada (gelada baboon)

C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996

C:Accession: C28854

R:Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 94, 1973-1978, 1983

A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit

A:Reference number: A91973; MUID:84161822; PMID:6423621

A:Accession: C28854

A:Molecule type: protein

A:Residues: 1-16 <NAK>

C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.00076;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13

DB 5 EGDFLAEGGGVR 16

RESULT 3

A24180

fibrinogen alpha chain - Japanese macaque (fragment)

N:Contains: fibrinopeptide A

C;Species: Macaca fuscata (Japanese macaque)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 26-Jan-1996
C;Accession: A24180
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Haplorhina patas), and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: A24180
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | | | |
DB 5 EGDFLAEGGGVR 16

RESULT 4
B24180
fibrinogen alpha chain - red guenon (fragment)
N;Contains: fibrinopeptide A
C;Species: Erythrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C;Accession: B24180
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Haplorhina patas), and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: B24180
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | | | |
DB 5 EGDFLAEGGGVR 16

RESULT 5
A28854
fibrinopeptide A - olive baboon
C;Species: Papio hamadryas anubis (olive baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: A28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus).
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: A28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | | | |
DB 5 EGDFLAEGGGVR 16

RESULT 6
A28854
fibrinopeptide A - olive baboon
C;Species: Papio hamadryas anubis (olive baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: A28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus).
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: A28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

B28854
fibrinopeptide A - hamadryas baboon
C;Species: Papio hamadryas (hamadryas baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: B28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus).
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: B28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | | | |
DB 5 EGDFLAEGGGVR 16

RESULT 7
A29501
fibrinopeptide A - baboon
C;Species: Papio sp. (baboon)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
C;Accession: A29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
Unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serology of Baboons.
A;Reference number: A29501
A;Accession: A29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | | | |
DB 5 EGDFLAEGGGVR 16

RESULT 8
FGHUA
fibrinogen alpha chain precursor, short splice form [validated] - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1987 #text_change 08-Dec-2000
C;Accession: A93956; A43568; I84456; A44234; C44234; B94433; A90433; B94309; S192
R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A;Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: evolution and expression.
A;Reference number: A93956; MUID:83247396; PMID:6575389
A;Accession: A93956
A;Molecule type: mRNA
A;Residues: 1-644 <KAN>
A;Cross-references: GB:J00128; NID:q182425; PIDN:AAA52427.1; PID:q182426
A;Note: the authors translated the codon GAG for residue 247 as Gly, GGA for residue 438
R;Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A;Reference number: A43568; MUID:91344740; PMID:2102623
A;Accession: A43568
A;Molecule type: DNA
A;Residues: 1-330, 'A', 332-644 <CHU>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
R;Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.

Biochemistry 22, 3237-3244, 1983
A:Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha A:Reference number: A90468; MUID:83283432; PMID:6688355
A:Accession: A90468
A:Molecule type: mRNA
A:Residues: 1-330, 'N', 332-629 <RIX>
A:Cross-references: GB:J00127; NID:g182423; PIDN:AAA52426.1; PID:g182424
R:Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A:Title: Isolation and characterization of cDNA clones for the Aalpha- and gamma-chains A:Reference number: I37393; MUID:84069777; PMID:6689067
A:Accession: I84456
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 110-156 <RES>
A:Cross-references: GB:K02272; NID:g182427; PIDN:AAA52428.1; PID:g182428
R:Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma Biochemistry 31, 11968-11972, 1992
A:Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel A:Reference number: A44234; MUID:93090725; PMID:1457396
A:Accession: A44234
A:Molecule type: mRNA
A:Residues: 1-51 <FU>
A:Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A>Note: sequence extracted from NCBI backbone (NCBIN:119912, NCBIN:119914, NCBIN:119918) A:Accession: C44234
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 605-644 <FU2>
A:Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A>Note: sequence extracted from NCBI backbone (NCBIP:119920)
R:Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v A:Reference number: A94433
A:Accession: B94433
A:Molecule type: protein
A:Residues: 20-214, 'RS', 217-298, 'G', 300-303, 'G', 305-629 <HEN>
R:Watt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
Biochemistry 18, 5410-5416, 1979
A:Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Overlappin A:Reference number: A90433; MUID:80088231; PMID:518846
A:Contents: disulfide bonds
A:Accession: A90433
A:Molecule type: protein
A:Residues: 20-146, 'Q', 148-195, 'N', 197-230, 'N', 232-316, 'SG', 319-406, 'D', 408, 'N', 410-629 R:Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080; PMID:936108
A:Contents: variant, and disulfide bonds
A:Accession: B94309
A:Molecule type: protein
A:Residues: 20-65, 'T', 67-629 <BLO>
R:Dewey, R.S.; Liesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumford Biochem. J. 281, 519-524, 1992
A:Title: Purification and characterization by fast-atom-bombardment mass spectrometry of incubation with calcium ionophore A23187.
A:Reference number: S19297; MUID:92143822; PMID:1736899
A:Accession: S19297
A:Molecule type: protein
A:Residues: 20-40 <DEW>
R:Retzius, A.D.; Markland Jr., F.S.
Thromb. Res. 52, 541-552, 1988
A:Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co A:Reference number: A60905; MUID:89162316; PMID:3232124
A:Accession: A60905
A:Molecule type: protein
A:Residues: 433-451 <RET>
R:Freto, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
J. Biol. Chem. 253, 2184-2195, 1978
A:Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin. A:Reference number: A92225; MUID:78130085; PMID:632262

A:Contents: annotation; cross-linking acceptor sites
R:Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.
Biochemistry 18, 5405-5410, 1979
A:Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locati A:Reference number: A90433; MUID:80088230; PMID:518845
A:Contents: annotation; cross-linking acceptor sites
R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Reference number: A90037; MUID:83254370; PMID:6575689
A:Contents: annotation; review, disulfide bonds
R:Itarte, E.; Plana, M.; Guasch, M.D.; Martos, C.
Biochem. Biophys. Res. Commun. 117, 631-636, 1983
A:Title: Phosphorylation of fibrinogen by casein kinase 1.
A:Reference number: A90116; MUID:84104274; PMID:6318767
A:Contents: annotation; phosphorylation
A>Note: about one-third of alpha chain molecules in blood were found to be phosphorylated R:Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751; PMID:6383194
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Kimura, S.; Aoki, N.
J. Biol. Chem. 261, 15591-15595, 1986
A:Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A:Reference number: A92565; MUID:87057190; PMID:2877981
A:Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
R:Krishnamurthi, S.; Dickens, T.A.; Patel, Y.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
A:Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of protei A:Reference number: A33261; MUID:89392031; PMID:2783136
A:Contents: annotation; activity of cell attachment (R-G-D) motif
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-ter A:Reference number: A37117; MUID:90337977; PMID:2143188
A:Contents: annotation; hementin cleavage site
R:Staecker, L.; Sillard, R.; Bensch, K.W.; Ruf, A.; Raida, M.; Schulz-Knappe, P.; Schep Biochem. Biophys. Res. Commun. 215, 896-902, 1995
A:Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites an A:Reference number: JC4334; MUID:96027996; PMID:748058
A:Contents: annotation; composition and amino-terminal sequences of carboxyl end peptides C:Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
C:Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Comment: See PIR:D44234 for the minor alternative splice form.
C:Genetics:
A:Gene: GDB:PGA
A:Cross-references: GDB:119129; OMIM:134820
A:Map position: 4q28-4q28
A:Introns: 18/3; 60/3; 122/1; 171/2
A>Note: the list of introns is incomplete
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see f ins are contained in the core. Two three-chain coiled coils emerge from this core and cor from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into f A:Pathway: blood coagulation
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C:Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein; liver; p; p F1-19/Domains: signal sequence #status predicted <SIG>
F20-629/Product: fibrinogen alpha chain #status experimental <APT>
F20-35/Product: fibrinopeptide A #status experimental <PGA>
F36-629/Product: fibrin alpha chain #status experimental <FGA>
F36-38/Region: polymerization site, binding to the distal domain of the gamma chain of F57-185/Domains: fibrinogen disulfide ring homology <FDR>
F591-593/Region: cell attachment (R-G-D) motif
F22,460/Binding site: phosphate (Ser) (covalent) #status experimental

F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
 F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
 F;55/Disulfide bonds: interchain (to beta-95) #status experimental
 F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
 F;68/Disulfide bonds: interchain (to beta-106) #status experimental
 F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
 F;184/Disulfide bonds: interchain (to beta-223) #status experimental
 F;288.419/Binding site: carbohydrate (Asn) (covalent) #status absent
 F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
 F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
 F;461-491/Disulfide bonds: #status experimental
 F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status

Query Match 87.78; Score 57; DB 1; Length 644;
 Best Local Similarity 91.7%; Pred. No. 0.039; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 24 EGDFLAEGGGVR 35

RESULT 9

D44234
 fibrinogen alpha chain precursor, extended splice form - human
 N;Alternate names: coagulation factor I
 N;Contains: fibrinopeptide A
 C;Species: Homo sapiens (man)
 C;Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
 C;Accession: D44234
 R;Fu, Y.; Weisbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
 Biochemistry 31, 11968-11972, 1992
 A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel
 A;Reference number: A44234; PMID:1457396
 A;Accession: D44234
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA; DNA
 A;Residues: 1-866 <FU>
 A;Cross-references: GB:M58569; NID:g182406; PID:g182407
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown
 A;Accession: B44234
 A;Molecule type: mRNA; DNA
 A;Residues: 605-866 <FU2>
 A;Note: sequence extracted from NCBI backbone (NCBIP:11917)
 C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
 C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
 ization sites responsible for the formation of the soft clot.
 C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
 ger) and between alpha chains (weaker) of different monomers.
 C;Comment: All fibrinogen chains are synthesized in the liver.
 C;Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
 C;Genetics:
 A;Gene: GDB:FGA
 A;Cross-references: GDB:119129; OMIM:134820
 A;Map position: 4q28-4q28
 A;Introns: 18/3; 60/3; 122/1; 171/2
 A;Note: the list of introns is incomplete
 C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentical
 tained in the core. Two three-chain coiled coils emerge from this core and connect it to
 distal domain nodes.
 C;Function:
 A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A;Pathway: blood coagulation
 C;Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
 C;Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
 F;20-35/Product: fibrinopeptide A #status experimental <APT>
 F;36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
 F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
 F;591-593/Region: cell attachment (R-G-D) motif
 F;629-863/Domain: fibrinogen beta/gamma homology <FBG>
 F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental

F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
 F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
 F;55/Disulfide bonds: interchain (to beta-95) #status experimental
 F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
 F;68/Disulfide bonds: interchain (to beta-106) #status experimental
 F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
 F;184/Disulfide bonds: interchain (to beta-223) #status experimental
 F;288.419/Binding site: carbohydrate (Asn) (covalent) #status absent
 F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
 F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
 F;461-491/Disulfide bonds: #status experimental
 F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
 F;686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.78; Score 57; DB 2; Length 866;
 Best Local Similarity 91.7%; Pred. No. 0.053; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 24 EGDFLAEGGGVR 35

RESULT 10

F29501
 fibrinopeptide A - wombat
 C;Species: Vombatidae gen. sp. (wombat)
 C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
 C;Accession: F29501
 R;Blombaeck, B.; Blombaeck, M.; Hann, C.
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
 A;Reference number: A29501
 A;Accession: F29501
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <BLO>
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 80.0%; Score 52; DB 2; Length 15;
 Best Local Similarity 76.9%; Pred. No. 0.0055; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
 : | | | | | | | | | |
 Db 3 TEGSFLAEGGGVR 15

RESULT 11

G29501
 fibrinopeptide A - bear
 C;Species: Ursus sp. (bear)
 C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
 R;Blombaeck, B.; Blombaeck, M.; Hann, C.
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
 A;Reference number: A29501
 A;Accession: G29501
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-16 <BLO>
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 78.5%; Score 51; DB 2; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 2; Indels 0; Gaps 0;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGEFLAEGGGVR 16

RESULT 12

A05296

fibrinogen alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996
C:Accession: A94308; A03118; A37511; A05296; B37511; C03118
R:Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A:Title: Studies of the structure of canine fibrinogen.
A:Reference number: A94308; MUID:76081726; PMID:1198547
A:Accession: A94308
A:Molecule type: protein
A:Residues: 1-28 <BIR>
R:Blombaeck, B.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A:Title: Studies on fibrinopeptides from mammals.
A:Reference number: A03118
A:Accession: A03118
A:Molecule type: protein
A:Residues: 1-16 <BLO>
R:Osbaahr Jr., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.
Biochem. Biophys. Res. Commun. 14, 555-558, 1964
A:Reference number: A37511; MUID:66020594; PMID:5836555
A:Accession: A37511
A:Molecule type: protein
A:Residues: 1, D', 3, 'EGKQ', 8-16 <OSB>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C:Keywords: blood coagulation; liver; phosphoprotein; plasma
F:1-16/Product: fibrinopeptide A #status experimental <APT>
F:3/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 78.5%; Score 51; DB 2; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.016;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
DB 5 EGEFLAEGGGVR 16

RESULT 13
E29501
fibrinopeptide A - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C:Accession: E29501
R:Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: E29501
A:Molecule type: protein
A:Residues: 1-17 <BLO>
R:Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A:Title: Studies on fibrinopeptides from mammals.
A:Reference number: A03118
A:Contents: annotation; confirmation of species assignment
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 75.4%; Score 49; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.022;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
DB 6 KGEFLAEGGGVR 17

RESULT 14
I29501
fibrinopeptide A - kangaroo
C:Species: Macropus sp. (kangaroo)
C:Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C:Accession: I29501
R:Blombaeck, B.; Blombaeck, M.; Hann, C.

unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: I29501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <BLO>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 73.8%; Score 48; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 0.029;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
DB 4 EGTFLAEGGGVR 15

RESULT 15
B29501
fibrinopeptide A - European moose
C:Species: Alces alces alces (European moose, elk)
C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C:Accession: B29501
R:Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: B29501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <BLO>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 73.8%; Score 48; DB 2; Length 19;
Best Local Similarity 90.0%; Pred. No. 0.037;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DFLAEGGGVR 13
DB 10 EFLAEGGGVR 19

Search completed: April 27, 2004, 16:24:55
Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2004, 16:22:47 ; Search time 11 Seconds
(without alignments)

61.537 Million cell updates/sec

Title: US-09-845-729A-1_COPY_2_14

Perfect score: 65

Sequence: 1 SESDFLAEGGVR 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	87.7	16	1 FIBA_MACFU	P12803 macaca fusc
2	57	87.7	19	1 FIBA_CREEL	P14446 cervus elap
3	57	87.7	866	1 FIBA_HUMAN	P02671 homo sapien
4	56	86.2	16	1 FIBA_CERSI	P14535 ceratotheri
5	54	83.1	16	1 FIBA_TAPTE	P14536 tapirus ter
6	53	81.5	16	1 FIBA_HYLLA	P14453 hylobates l
7	53	81.5	18	1 FIBA_CAMDR	P14444 camelus dro
8	53	81.5	19	1 FIBA_BISBO	P14441 bison bonas
9	53	81.5	19	1 FIBA_CERNI	P14447 cervus nipp
10	51	78.5	16	1 FIBA_FELCA	P14450 felis silve
11	51	78.5	28	1 FIBA_CANFA	P02673 canis fami
12	49	75.4	17	1 FIBA_PIG	P14460 sus scrofa
13	49	75.4	18	1 FIBA_LANGL	P14454 lama glama
14	48	73.8	15	1 FIBA_SYNCA	P14463 syncerus ca
15	48	73.8	16	1 FIBA_EQVAS	P14449 equus asinu
16	48	73.8	16	1 FIBA_MANLE	P14455 mandrillus
17	48	73.8	16	1 FIBA_ODOHE	P14459 odocoileus
18	48	73.8	19	1 FIBA_BUBBU	P14442 bubalus bub
19	48	73.8	19	1 FIBA_SHEEP	P14451 ovis aries
20	48	73.8	596	1 FIBA_BOVIN	P02672 bos taurus
21	47	72.3	14	1 FIBA_HORSE	P14452 equus cabal
22	45	69.2	19	1 FIBA_MUNMU	P14457 muntiacus m
23	41	63.1	271	1 PANB_XANAC	O8pl11 xanthomonas
24	41	63.1	271	1 PANB_XANCP	O8p9t0 xanthomonas
25	40	61.5	15	1 FIBA_ANAPL	P12801 anas platyr
26	40	61.5	1696	1 PKC5_BRACL	O9nj15 branchiosto
27	39	60.0	13	1 FIBA_CAVPO	P14445 cavia porce
28	39	60.0	236	1 IPT_PANAY	O47851 pantoea agg
29	39	60.0	271	1 AAC3_PSEAE	P29808 pseudomonas
30	38	58.5	611	1 IF4B_HUMAN	P23588 homo sapien
31	38	58.5	717	1 U84B_HUMAN	O9uh99 homo sapien
32	37	56.9	19	1 FIBA_RANTA	P14462 rangifer ta
33	37	56.9	413	1 IDHC_SOYBN	Q06197 glycine max

RESULT 1

ID	FIBA_MACFU	STANDARD;	PRT;	16 AA.
AC	P12803;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Fibrinogen alpha chain (Contains: Fibrinopeptide A) (Fragment).			
GN	FGA.			
OS	Macaca fuscata fuscata (Japanese macaque),			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey),			
OS	Macaca mulatta (Rhesus macaque),			
OS	Cercopithecus aethiops (Green monkey) (Grivet),			
OS	Erythrocebus patas (Red guenon) (Hussar),			
OS	Papio anubis (Olive baboon),			
OS	Papio hamadryas (Hamadryas baboon), and			
OS	Theropithecus gelada (Gelada baboon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC	Cercopitheciae; Macaca.			
OX	NCBI_TaxID=9543, 9541, 9544, 9534, 9538, 9555, 9557, 9565;			
RN	[1]			
RP	SEQUENCE.			
RC	SPECIES=E.patas, and M.fuscata;			
RX	MEDLINE=85289140; PubMed=3928610;			
RA	Nakamura S., Takenaka O., Takahashi K.;			
RT	"Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and			
RT	patas monkey (Erythrocebus patas): their amino acid sequences,			
RT	restricted mutations, and a molecular phylogeny for macaques,			
RT	guenons, and baboons.";			
RL	J. Biochem. 97:1487-1492(1985).			
RN	[2]			
RP	SEQUENCE.			
RC	SPECIES=P.anubis, P.hamadryas, and T.gelada;			
RX	MEDLINE=84161822; PubMed=6423621;			
RA	Nakamura S., Takenaka O., Takahashi K.;			
RT	"Fibrinopeptides A and B of Baboons (Papio anubis, Papio hamadryas,			
RT	and Theropithecus gelada): their amino acid sequences and			
RT	evolutionary rates and a molecular phylogeny for the baboons.";			
RL	J. Biochem. 94:1973-1978(1983).			
RN	[3]			
RP	SEQUENCE.			
RC	SPECIES=C.aethiops, M.mulatta, and M.fascicularis;			
RA	Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;			
RT	"Studies on fibrinopeptides from primates.";			
RT	Acta Chem. Scand. 19:1789-1789(1965).			
CC	-!- FUNCTION: Fibrinogen has a double function: yielding monomers that			
CC	polymerize into fibrin and acting as a cofactor in platelet			
CC	aggregation.			
CC	-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS			
CC	(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.			
CC	-!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,			
CC	which cleaves fibrinopeptides A and B from alpha and beta chains,			
CC	and thus exposes the N-terminal polymerization sites responsible			
CC	for the formation of the soft clot.			
DR	PIR; A24180; A24180.			

P50218 nicotiana t
P50217 solanum tub
P42084 bacillus su
Q8k5m2 streptococ
Q8nz53 streptococ
P58080 streptococ
Q40345 medicago sa
Q9nqcl homo sapien
P14458 mustela vis
Q8why4 psilotum nu
Q9pgr9 xylella fas
Q87ew0 xylella fas

ALIGNMENTS

DR PIR; A28854; A28854.
 DR PIR; B24180; B24180.
 DR PIR; B28854; B28854.
 DR PIR; C28854; C28854.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1551 MW; 49B8CB63EA04DD3 CRC64;

Query Match 87.7%; Score 57; DB 1; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00075;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEGGGVR 16

RESULT 2

FIBA_CEREL STANDARD; PRT; 19 AA.

AC P1446;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.

OS Cervus elaphus (Red deer), and
 OS Cervus elaphus nelsoni (American elk).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860, 9864;

RN [1]

RP SEQUENCE.

RC SPECIES=C.elaphus;
 RA Blomback B., Blomback M., Grondahl N.J.;
 RA "Studies on fibrinopeptides from mammals.";
 RT Acta Chem. Scand. 19:1789-1791(1965).
 RN [2]

RN SEQUENCE.

RC SPECIES=C.e.nelsoni;

RA Moss G.A., Doolittle R.F.;

RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";

RL Arch. Biochem. Biophys. 122:674-684(1967).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.

CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.

KW Blood coagulation; Plasma.

FT PEPTIDE 1 19 FIBRINOPEPTIDE A.

FT NON_TER 19 19

SQ SEQUENCE 19 AA; 1808 MW; 9BA54C26873B59C5 CRC64;

Query Match 87.7%; Score 57; DB 1; Length 19;
 Best Local Similarity 84.6%; Pred. No. 0.00088;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SESDFLAEGGGVR 13
 Db 7 ASSDFLAEGGGVR 19

RESULT 3

FIBR_HUMAN

ID FIBA_HUMAN STANDARD; PRT; 866 AA.

AC P02671; Q9UBX2; Q9UCH2;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A].
 GN FGA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
 RX MEDLINE=93090725; PubMed=1457396;
 RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
 RA Roy S.N., Redman C.M., Grieninger G.;
 RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
 RT subunit: a novel exon conferring marked homology to beta and gamma
 RT subunits.";
 RL Biochemistry 31:11968-11972(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
 RX Chung D.W., Grieninger G.;
 RA "Fibrinogen DNA and protein sequences.";
 RT (in) Ebert R.F. (eds.);
 RL Index of variant human fibrinogens, pp.13-24, CRC Press,
 RL Boca Raton (1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
 RP ALA-456.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted [JUN-2001] to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-655 FROM N.A. (ISOFORM ALPHA-E).
 RC TISSUE=Liver;
 RX MEDLINE=9134740; PubMed=2102623;
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 RT fibrinogen.";
 RL Adv. Exp. Med. Biol. 281:39-48(1990).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=83247396; PubMed=6575389;
 RA Kant J.A., Lord S.T., Crabtree G.R.;
 RT "Partial mRNA sequences for human A alpha, B beta, and gamma
 RT fibrinogen chains: evolutionary and functional implications.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
 RN [6]
 RP SEQUENCE OF 1-629 FROM N.A.
 RX MEDLINE=83283432; PubMed=6688355;
 RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT the alpha chain of human fibrinogen.";
 RL Biochemistry 22:3237-3244(1983).
 RN [7]
 RP SEQUENCE OF 20-629.
 RA Henschen A., Lottepeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants.";
 RL (in) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [8]
 RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
 RX MEDLINE=80088231; PubMed=518846;
 RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
 RT Overlapping sequences providing the complete sequence.";
 RL Biochemistry 18:5410-5416(1979).
 RN [9]
 RP SEQUENCE OF 110-156 FROM N.A.
 RX MEDLINE=84069777; PubMed=6689067;
 RA Imam A.M., Eaton M.A., Williamson R., Humphries S.;
 RT "Isolation and characterisation of cDNA clones for the A alpha- and
 RT gamma-chains of human fibrinogen.";

RL Nucleic Acids Res. 11:7427-7434(1983).
RN [10]
RP SEQUENCE OF 605-644 FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=83254384; PubMed=6575700;
RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
RT "Cloning of fibrinogen genes and their cDNA.";
RL Ann. N.Y. Acad. Sci. 408:449-456(1983).
RN [11]
RP SEQUENCE OF 20-35.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
RN [12]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=80088230; PubMed=518845;
RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen."
RT Exact location of cross-linking acceptor sites.";
RL Biochemistry 18:5405-5410(1979).
RN [13]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=78130085; PubMed=632262;
RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RT "Localization of the alpha-chain cross-link acceptor sites of human fibrin.";
RL J. Biol. Chem. 253:2184-2195(1978).
RN [14]
RP VARIANT, AND DISULFIDE BONDS.
RX MEDLINE=76225080; PubMed=936108;
RA Blomback B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL Thromb. Res. 8:639-658(1976).
RN [15]
RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RT "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
RN [16]
RP CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
RX MEDLINE=87057190; PubMed=287798;
RA Kimura S., Aoki N.;
RT "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
RL J. Biol. Chem. 261:15591-15595(1986).
RN [17]
RP PHOSPHORYLATION.
RX MEDLINE=84104274; PubMed=6318767;
RA Itarte E., Plana M., Guasch M.D., Martos C.;
RT "Phosphorylation of fibrinogen by casein kinase 1.";
RL Biochem. Biophys. Res. Commun. 117:631-636(1983).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
RX MEDLINE=92218459; PubMed=1560020;
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT "The structure of residues 7-16 of the A alpha-chain of human fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.
RX MEDLINE=97472408; PubMed=9333233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.

RX MEDLINE=98356117; PubMed=9689040;
RA Spraggon G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian L., Redman C., Doolittle R.F., Grieninger G.;
RT "Crystal structure of a recombinant alphaEC domain from human fibrinogen-420.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
RN [22]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL Biochemistry 38:2941-2946(1999).
RN [23]
RP VARIANT KYOTO-2.
RX MEDLINE=91300048; PubMed=2070049;
RA Yoshida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule, characterized by the replacement of A alpha proline-18 by leucine.";
RL Blood 78:149-153(1991).
RN [24]
RP VARIANT LIMA.
RX MEDLINE=92340680; PubMed=1634621;
RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H., Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H., Perez-Requejo J.L., Matsuda M.;
RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A alpha-arginine-141 to serine substitution associated with extra N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel formation but normal fibrin-facilitated plasminogen activation catalyzed by tissue-type plasminogen activator.";
RL J. Clin. Invest. 90:67-76(1992).
RN [25]
RP VARIANT CARACAS-2.
RX MEDLINE=91268018; PubMed=1675636;
RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H., Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A., Arocha-Pinango C.L., Matsuda M.;
RT "An A alpha Ser-434 to N-glycosylated Asn substitution in a dysfibrinogen, fibrinogen Caracas II, characterized by impaired fibrin gel formation.";
RL J. Biol. Chem. 266:11575-11581(1991).
RN [26]
RP VARIANT DUSART.
RX MEDLINE=93232289; PubMed=8473507;
RA Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosesson M.W., Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C., Caen J.P.;
RT "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and its association with abnormal fibrin polymerization and thrombophilia.";
RN [27]
RP QUERY MATCH
QY 2 ESDFLAEGGVR 13
DB 24 EGDFLAEGGVR 35
Query Match 87.7%; Score 57; DB 1; Length 866;
Best Local Similarity 91.7%; Pred. No. 0.036;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 4
FIBA CERST
ID FIBA CERST STANDARD; PRT; 16 AA.
AC P14535;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.

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OK NCBI_TaxID=9807;
RN SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC Blood coagulation; Plasma.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1639 MW; 0958CBB6293F4C81 CRC64;

Query Match 86.2%; Score 56; DB 1; Length 16;
Best Local Similarity 76.9%; Pred. No. 0.0011;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
Db : : : : :
4 TEGDFIAEGGGVR 16

RESULT 5
FIBA_TAPTE STANDARD; PRT; 16 AA.
AC P14536;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Tapirus terrestris (Lowland tapir) (Brazilian tapir)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9801;
RN SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC Blood coagulation; Plasma.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1622 MW; 48598EB6292F4030 CRC64;

Query Match 83.1%; Score 54; DB 1; Length 16;
Best Local Similarity 76.9%; Pred. No. 0.0025;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
Db : : : : :
4 TEGDFIAEGGGVR 16

RESULT 6
FIBA_HYLLA STANDARD; PRT; 16 AA.

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AC P1453;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN SEQUENCE.
RA MEDLINE=70294424; PubMed=5466708;
RT "Gibbon fibrinopeptides: identification of a glycine-serine allelism
RT at position B-3."
RL Science 170:468-470(1970).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC Blood coagulation; Plasma.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1565 MW; 49E98EB63EA04DD3 CRC64;

Query Match 81.5%; Score 53; DB 1; Length 16;
Best Local Similarity 83.3%; Pred. No. 0.0037;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
Db : : : : :
5 EGEFLAEGGGVR 16

RESULT 7
FIBA_CAMDR STANDARD; PRT; 18 AA.
AC P14474;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN SEQUENCE.
RA MEDLINE=67209145; PubMed=6033721;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT Dromedary camel, mule deer, and cape buffalo."
RL Arch. Biochem. Biophys. 118:456-467(1967).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC Blood coagulation; Plasma.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 18 FIBRINOPEPTIDE A.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1835 MW; 244448763D7F4CC6 CRC64;

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Query Match      81.5%; Score 53; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0042;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
   | : |||||
Db 7 EGEFLAEGGGVR 18

RESULT 8
FIBA BISBO
ID FIBA BISBO STANDARD; PRT; 19 AA.
AC P14447;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9902;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC and cleaves fibrinopeptides A and B from alpha and beta chains,
CC which exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 19 FIBRINOPEPTIDE A.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1836 MW; 9BA55A0F473B59C5 CRC64;

Query Match      81.5%; Score 53; DB 1; Length 19;
Best Local Similarity 76.9%; Pred. No. 0.0044;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
   | : |||||
Db 7 ASGDFLAEGGGVR 19

RESULT 9
FIBA CERNI
ID FIBA CERNI STANDARD; PRT; 19 AA.
AC P14447;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Cervus nippon (Sika deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9863;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
RT "Structure of fibrinopeptides-its relation to enzyme specificity and
RT phylogeny and classification of species.";
RL Ark. Kem. 25:411-428(1966).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that

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CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1822 MW; 9BA40926873B59C5 CRC64;

Query Match      81.5%; Score 53; DB 1; Length 19;
Best Local Similarity 76.9%; Pred. No. 0.0044;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
   | : |||||
Db 7 ASSEFLAEGGGVR 19

RESULT 10
FIBA FELCA
ID FIBA FELCA STANDARD; PRT; 16 AA.
AC P14450;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1620 MW; C3C98EB62D6CC7D3 CRC64;

Query Match      78.5%; Score 51; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.0084;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
   | : |||||
Db 5 EGEFLAEGGGVR 16

RESULT 11
FIBA CANFA
ID FIBA CANFA STANDARD; PRT; 28 AA.
AC P02673; P14464;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Canis familiaris (Dog), and
OS Vulpes vulpes (Red fox).

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615, 9627;
RN [1]
RN SEQUENCE.
RC SPECIES=C.familiaris;
RA MEDLINE=76081726; PubMed=1198547;
RX Birken S., Wilner G.D., Canfield R.E.;
RT "Studies of the structure of canine fibrinogen.";
RL Thromb. Res. 7:599-610(1975).
RN [2]
RN SEQUENCE OF 1-16.
RC SPECIES=C.familiaris, and V.vulpes;
RA Blomback B., Blomback M., Grondahl N.J.;
RX "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [3]
RN SEQUENCE OF 1-16.
RC SPECIES=C.familiaris;
RA MEDLINE=66020594; PubMed=5836555;
RX Osbahr A.J. Jr., Colman R.W., Laki K., Gladner J.A.;
RT "The nature of the peptides released from canine fibrinogen.";
RL Biochem. Biophys. Res. Commun. 14:555-558(1964).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; A94308; A05296.
KW Blood coagulation; Plasma; Phosphorylation.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT MOD RES 3 3 PHOSPHORYLATION (PARTIAL).
FT CONFLICT 2 2 N -> D (IN REF. 2).
FT CONFLICT 4 7 KEGE -> EGKQ (IN REF. 2).
FT NON TER 28 28
SQ SEQUENCE 28 AA; 2958 MW; 09DCD3F923BFBD2 CRC64;
Query Match 78.5%; Score 51; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.014;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ESDFLAEGGGVR 13
DB 5 EGEFIAEGGGVR 16
RESULT 12
FIBA_PIG
ID FIBA_PIG STANDARD; PRT; 17 AA.
AC P14460;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RX "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; E29501; E29501.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1762 MW; 232EFEBB8B6B0A0C CRC64;
Query Match 75.4%; Score 49; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.02;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ESDFLAEGGGVR 13
DB 6 KGEFLAEGGGVR 17
RESULT 13
FIBA_LAMGL
ID FIBA_LAMGL STANDARD; PRT; 18 AA.
AC P14454;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Lama glama (Llama), and
OS Lama vicugna (Vicugna) (Vicugna vicugna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844, 9843;
RN [1]
RN SEQUENCE.
RC SPECIES=L.glama;
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [2]
RN SEQUENCE.
RC SPECIES=L.vicugna;
RA Moss G.A., Doolittle R.P.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";
RL Arch. Biochem. Biophys. 122:674-684(1967).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 18 FIBRINOPEPTIDE A.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1834 MW; 2444487B8B7F4CC6 CRC64;
Query Match 75.4%; Score 49; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.021;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ESDFLAEGGGVR 13
DB 7 KGEFLAEGGGVR 18
RESULT 14
FIBA_SYNCA
ID FIBA_SYNCA STANDARD; PRT; 15 AA.
AC P14463;
DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Syncerus caffer (Cape buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Syncerus.
 OX NCBI_TaxID=9970;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=67209145; PubMed=6033721;
 RA Doilittle R.F., Schubert D., Schwartz S.A.;
 RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
 RT Dromedary camel, mule deer, and cape buffalo.";
 RL Arch. Biochem. Biophys. 118:456-467(1967).
 CC -I- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -I- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -I- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1480 MW; 4E998EASFOB41CC6 CRC64;

 Query Match 73.8%; Score 48; DB 1; Length 15;
 Best Local Similarity 90.0%; Pred. No. 0.026;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 4 DFLAEGGGVR 13
 DB :|||||||
 6 EFLAEGGGVR 15

 RESULT 15
 FIBA EQUAS
 ID_FIBA_EQUAS STANDARD; PRT; 16 AA.
 AC P14449;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Equus asinus (Donkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9793;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -I- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -I- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -I- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1696 MW; 09598EB63C2A5957 CRC64;

 Query Match 73.8%; Score 48; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.028;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13

Db 5 EGEFISEGGGVR 16

Search completed: April 27, 2004, 16:24:21
Job time : 11 secs

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OM protein - protein search, using sw model

Run on: April 27, 2004, 16:22:48 ; Search time 39 Seconds
(without alignments)
105.173 Million cell updates/sec

Title: US-09-845-729a-1_COPY_2_14
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	57	87.7	218	4	Q8W76	Q8W76 homo sapien
2	46	70.8	557	11	Q99K47	Q99K47 mus musculus
3	43	66.2	260	10	Q8S2N9	Q8S2N9 oryza sativ
4	41	63.1	242	5	Q8T925	Q8T925 tetrahymena
5	41	63.1	552	2	Q9APX1	Q9APX1 pseudomonas
6	40	61.5	280	16	Q99WM6	Q99WM6 staphylococ
7	40	61.5	280	16	Q8NY96	Q8NY96 staphylococ
8	40	61.5	401	10	Q8S0S5	Q8S0S5 oryza sativ
9	40	61.5	630	13	Q8UW15	Q8UW15 lapemis har
10	40	61.5	852	5	Q9U4G5	Q9U4G5 drosophila
11	39	60.0	89	16	Q9BF73	Q9BF73 rhizobium 1
12	39	60.0	171	3	Q9P8L5	Q9P8L5 botrytis ci
13	39	60.0	186	2	Q9F7D5	Q9F7D5 salmonella
14	39	60.0	245	16	Q9Z4S4	Q9Z4S4 salmonella
15	39	60.0	245	16	Q8Z6K4	Q8Z6K4 salmonella
16	39	60.0	324	16	O53481	O53481 mycobacteri.

17	39	60.0	324	16	Q7TZ37	Q7TZ37 mycobacteri
18	39	60.0	365	16	Q823I9	Q823I9 chlamydomphi
19	39	60.0	450	16	Q8P973	Q8P973 xanthomonas
20	39	60.0	462	10	Q8LFX3	Q8LFX3 arabidopsis
21	39	60.0	465	10	Q9LH81	Q9LH81 arabidopsis
22	39	60.0	465	10	Q940V4	Q940V4 arabidopsis
23	39	60.0	481	10	Q8W0R4	Q8W0R4 sorghum bic
24	39	60.0	546	5	Q9VHD0	Q9VHD0 drosophila
25	39	60.0	580	10	Q7XN79	Q7XN79 oryza sativ
26	39	60.0	705	2	O85866	O85866 sphingomona
27	39	60.0	748	10	Q8W0N1	Q8W0N1 oryza sativ
28	39	60.0	753	10	Q9LIC9	Q9LIC9 arabidopsis
29	39	60.0	753	10	Q8L741	Q8L741 arabidopsis
30	39	60.0	1159	4	Q9NY34	Q9NY34 homo sapien
31	39	60.0	1165	4	Q9NZQ8	Q9NZQ8 homo sapien
32	38.5	59.2	741	16	Q8UFY1	Q8UFY1 agrobacteri
33	38	58.5	77	10	Q84S45	Q84S45 aster tripo
34	38	58.5	99	16	Q8ZQ92	Q8ZQ92 salmonella
35	38	58.5	147	10	Q9MAV0	Q9MAV0 arabidopsis
36	38	58.5	155	16	Q8ELS7	Q8ELS7 oceanobacil
37	38	58.5	195	16	Q8EAT0	Q8EAT0 shewanella
38	38	58.5	256	16	Q92LM7	Q92LM7 rhizobium m
39	38	58.5	548	2	Q845J1	Q845J1 pseudomonas
40	38	58.5	575	10	Q8H147	Q8H147 arabidopsis
41	38	58.5	575	10	Q9LZM8	Q9LZM8 arabidopsis
42	38	58.5	575	10	Q8LGGJ2	Q8LGGJ2 arabidopsis
43	38	58.5	611	4	Q8WVK5	Q8WVK5 homo sapien
44	38	58.5	611	11	Q8BGD9	Q8BGD9 mus musculu
45	38	58.5	652	16	Q8YPV7	Q8YPV7 anabaena sp

ALIGNMENTS

RESULT 1

Q8W76	PRELIMINARY;	PRT;	218 AA.
ID	Q8W76		
AC	Q8W76		
DT	01-MAR-2002 (Tremblrel. 20, Created)		
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)		
DT	01-MAR-2002 (Tremblrel. 20, Last annotation update)		
DE	Similar to fibrinogen, A alpha polypeptide.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RA	Strausberg R.;		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC020764; AAH20764.1; -		
SQ	SEQUENCE 218 AA; 24695 MW; 36D756A8116EA94A CRC64;		

Query Match 87.7%; Score 57; DB 4; Length 218;
Best Local Similarity 91.7%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2

Q99K47	PRELIMINARY;	PRT;	557 AA.
ID	Q99K47		
AC	Q99K47		
DT	01-JUN-2001 (Tremblrel. 17, Created)		
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)		
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)		
DE	Fibrinogen A alpha polypeptide.		
GN	FGA.		
OS	Mus musculus (Mouse).		

RA Xu A., Wei J., Yang W., Zhao G., Zhong X.;
 RT "A novel eukaryotic translation initiation factor 4B cDNA clone from
 RT sea snake";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF165225; AAL54908.1; -
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00076; trm; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PSS0102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 SQ SEQUENCE 630 AA; 71186 MW; E3457B6ED3502A16 CRC64;
 Query Match 61.5%; Score 40; DB 13; Length 630;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 SDFLAEGGG 11
 |||||
 Db 18 SDFLAEDGG 26
 RESULT 10
 Q9U4G5 PRELIMINARY; PRT; 852 AA.
 AC Q9U4G5; OSVQB2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE BCDA:GH09817 protein.
 GN BCDA:GH09817 OR CG4272.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Teang G.,
 RA Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,
 RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
 RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
 RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
 RA Park S., Sequeira A., Sethi H., Snir E., Svirskaas R.R., Weinburg T.,
 RA Celniker S.E.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003583; AAF51264.1; ALT_INIT.
 DR EMBL; AF181640; AAD55426.1; -
 DR FlyBase; FBgn0028485; BCDA:GH09817.
 KW Hypothetical protein.
 SQ SEQUENCE 852 AA; 91073 MW; B87C3607203DA4EC CRC64;
 Query Match 61.5%; Score 40; DB 5; Length 852;
 Best Local Similarity 63.6%; Pred. No. 2.3e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 SESDFLAEGGG 11
 |||||
 Db 376 SEEDYLSEGG 386
 RESULT 11
 Q98F73 PRELIMINARY; PRT; 89 AA.
 AC Q98F73;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein ms13900.
 GN MS13900.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti";
 RL DNA Res. 7:331-338 (2000).
 DR EMBL; AF003003; BAB50694.1; -
 DR InterPro; IPR006339; ABRB_trans_reg.
 DR InterPro; IPR007159; SpoVT_ABRB.
 DR Pfam; PF04014; SpoVT_ABRB; 1.
 DR TIGRFAMs; TIGR01439; lp_hng_hel_ABRB; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 89 AA; 10058 MW; 5197B7CB06AFC351 CRC64;
 Query Match 60.0%; Score 39; DB 16; Length 89;
 Best Local Similarity 61.5%; Pred. No. 29;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 SESDFLAEGGGVR 13
 |||||
 Db 25 SEVEFVATDGGVR 37

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Q9Z4S4          Q9Z4S4      PRELIMINARY;       PRT;   245 AA.
ID    AC        Q9Z4S4;
AC     AC        Q9Z4S4;
DT     DT        01-MAY-1999 (TrEMBLrel. 10, Created)
DT     DT        01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT     DT        01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT     DT        ORF_245 protein (Putative cytoplasmic protein).
DE     DE        ORF245 OR STM1381.
GN     GN        Salmonella typhimurium.
OS     OS        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC     OC        Enterobacteriaceae; Salmonella.
OX     OX        NCBI_TaxID=602;
RN     [1]
RP     RP        SEQUENCE FROM N.A.
RC     RC        STRAIN=LT2;
RX     RX        MEDLINE=99157556; PubMed=10027956;
RA     RA        Hensel M., Egeleer C., Nikolaus T.;
RT     RT        "Molecular and functional analysis indicates a mosaic structure of
RL     RL        Salmonella Pathogenicity Island 2.";
RM     RM        Mol. Microbiol. 31:489-498(1999) .
RN     [2]
RP     RP        SEQUENCE FROM N.A.
RC     RC        STRAIN=LT2;
RX     RX        Hensel M., Hinsley A.P., Nikolaus T., Sawers G., Berks B.C.;
RT     RT        "he genetic basis of tetrathionate respiration in Salmonella
RL     RL        typhimurium.";
RM     RM        Mol. Microbiol. 0:0-0(0) .
RN     [3]
RP     RP        SEQUENCE FROM N.A.
RC     RC        STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX     RX        MEDLINE=21534948; PubMed=11677609;
RA     RA        McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RT     RT        Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA     Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA     Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA     RA        Ryan E., Wilson R.K.;
RT     RT        "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL     RL        LT2.";
RM     RM        Nature 413:852-856(2001) .
DR     DR        ENBL; AJ224978; CAB37418.1; -.
DR     DR        ENBL; AE008760; AAL20305.1; -.
DR     DR        InterPro; IPR003006; Ig_MHC.
DR     DR        PROSITE; PS00290; IG_MHC; 1.
KW     KW        Hypothetical protein; Complete proteome.
SQ     SQ        SEQUENCE 245 AA; 27430 MW; FFBF31AA9DC8E943 CRC64;

Query Match      60.0%; Score 39; DB 16; Length 245;
Best Local Similarity 60.0%; Pred.No. 88;
Matches      6; Conservative      4; Mismatches      0; Indels      0; Gaps

QY      3 SDFLAEGGV 12
Db      102 ADVAEGGL 111
           ::::|||||:

RESULT 15
Q8Z5K4          Q8Z5K4      PRELIMINARY;       PRT;   245 AA.
ID    AC        Q8Z5K4;
AC     AC        Q8Z5K4;
DT     DT        01-MAR-2002 (TrEMBLrel. 20, Created)
DT     DT        01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT     DT        01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE     DE        Orf_245 protein.
GN     GN        STY1741 OR TI249.
OS     OS        Salmonella typhi.
OC     OC        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC     OC        Enterobacteriaceae; Salmonella.
OX     OX        NCBI_TaxID=601;
RN     [1]
RP     RP        SEQUENCE FROM N.A.
RC     RC        STRAIN=CT18;
RX     RX        MEDLINE=21534947; PubMed=11677608;
RA     RA        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain

```

Search completed: April 27, 2004, 16:25:47
Job time : 39 secs

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OM protein - protein search, using sw model

Run on: April 27, 2004, 16:22:47 ; Search time 55 Seconds
(without alignments)
66.784 Million cell updates/sec

Title: US-09-845-729a-1_COPY_2_14
Perfect score: 65
Sequence: 1 SESDFLAEGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	13	6	ABG76139 Human alp
2	65	100.0	15	6	ABU08830 Alpha fib
3	65	100.0	15	6	ABG76138 Human alp
4	57	87.7	12	6	ABU09252 Human alp
5	57	87.7	13	6	ABU08825 Alpha fib
6	57	87.7	13	6	ADAI8539 Human alp
7	57	87.7	14	6	ABU08827 Alpha fib
8	57	87.7	16	2	AAR36194 Fibrinoge
9	57	87.7	16	2	AAW04619 Fibrinoge
10	57	87.7	16	2	AAV57487 Antimicro
11	57	87.7	16	4	ABBS6219 Fibrinoge
12	57	87.7	16	4	ABBS1959 Fibrinoge
13	57	87.7	16	4	ABBS2337 Human API
14	57	87.7	16	5	ABG73668 Linear HI
15	57	87.7	16	5	ABG78799 Multiple
16	57	87.7	16	5	ABG70000 Antimicro
17	57	87.7	16	5	ABG69911 Rabbit pl
18	57	87.7	16	5	ABP60019 Biopolyme
19	57	87.7	16	6	ABP60640 Fibrinoge
20	57	87.7	16	6	ADAI8542 Human alp
21	57	87.7	16	6	ABRS8740 Alzheimer
22	57	87.7	17	2	AAR36184 Fibrinoge
23	57	87.7	17	4	AAB31960 Fibrinoge
24	57	87.7	17	6	ABU08833 Alpha fib
25	57	87.7	17	6	ABU09101 Alpha fib

Aae34820 Staphyloc
Aar96193 Fibrinoge
Abu08834 Alpha fib
Abu08837 Alpha fib
Ada18541 Human alp
Aar96192 Fibrinoge
Aar96191 Fibrinoge
Aay57488 Antimicro
Abg69912 Rabbit pl
Aao27086 Fibrinoge
Aao27084 Fibrinoge
Aao27085 Fibrinoge
Aao27081 Fibrinoge
Aar96183 Fibrinoge
Aap90276 Antigen p
Aar96190 Fibrinoge
Aar96182 Fibrinoge
Aao21114 Anti-angi
Aao21113 Anti-angi
Aao21118 Anti-angi

ALIGNMENTS

RESULT 1
ABG76139
ID ABG76139 standard; peptide; 13 AA.
XX AC ABG76139;
XX DT 08-MAY-2003 (first entry)
XX DE Human alpha fibrinogen peptide #2.
XX KW Human; alpha fibrinogen; renal failure; myocardial infarction;
KW unstable angina; matrix assisted laser desorption-time of flight;
KW MALDI-TOF; mass spectroscopy; antigen.
XX OS Homo sapiens.
XX PN US2002160528-A1.
XX PD 31-OCT-2002.
XX PF 30-APR-2001; 2001US-00845729.
XX PR 30-APR-2001; 2001US-00845729.
(JACK/) JACKOWSKI G.
(THAT/) THATCHER B.
(MARS/) MARSHALL J.
(YANT/) YANTHA J.
(VREE/) VREES T.
Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
WPI; 2003-255194/25.
Novel biopolymer marker such as alpha fibrinogen having specific
molecular weight, useful in indicating disease state such as myocardial
infarction or renal failure.
Claim 1; Page 7; 10pp; English.
The invention relates a biopolymer marker such as alpha fibrinogen having
a molecular weight of about 1350 daltons and a sequence appearing as
CC ABG76139 useful in indicating at least one particular disease state. The
CC presence of the peptide in a sample is determined by matrix assisted
CC laser desorption-time of flight (MALDI-TOF) mass spectroscopy. The marker
CC is useful for indicating at least one particular disease state such as
CC myocardial infarction or renal failure (e.g. in a patient presenting with
CC unstable angina). The biopolymer marker is useful as antigen in

self.

CC immunoassays for the detection of those individuals suffering from the
CC disease known to be evidenced by the marker sequence. The biopolymer
CC marker rapidly and accurately diagnoses a disease state such as
CC myocardial infarction or renal failure, and allows physicians to identify
CC asymptomatic patients before they suffer from the disease state. The
CC present sequence is an alpha fibrinogen biopolymer marker
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 65; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
| | | | | | | | | |
DB 1 SESDFLAEGGGVR 13

RESULT 2

ABU08830
ID ABU08830 standard; peptide; 15 AA.

XX AC ABU08830;

XX DT 25-AUG-2003 (first entry)

XX DE Alpha fibrinogen peptide, #4, for physiological condition diagnostics.

XX KW Proteomic; human; physiological condition; analyte; biopolymer;
XX KM biomarker; alpha fibrinogen; renal failure; myocardial infarction; MI.

XX OS Homo sapiens.

XX PN US2002160420-A1.

XX PD 31-OCT-2002.

XX PF 30-APR-2001; 2001US-00846330.

XX PR 30-APR-2001; 2001US-00846330.

XX PA (JACK/) JACKOWSKI G.

XX PA (THAT/) THATCHER B.

XX PA (MARS/) MARSHALL J.

XX PA (YANT/) YANTHA J.

XX PA (VREE/) VREES T.

XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;

XX DR WPI; 2003-491923/46.

XX PT Determining proteomic basis e.g. basis for diagnosing existence of or
XX PT predicting development and/or progression of abnormal physiological
XX PT conditions based upon the presence of proteomic materials.

XX PS Disclosure; Page 12; 25pp; English.

XX CC The invention discloses a method for determining a proteomic basis for
XX CC development and progression of abnormal physiological conditions. The
XX CC method comprises isolating one or more patient specific proteomic
XX CC materials from a sample and comparing it against a library of proteomic
XX CC materials having characteristics identifiable with both normal and
XX CC abnormal physiological conditions or their predictive hallmarks. The
XX CC method is useful for determining a proteomic basis for development and
XX CC progression of abnormal physiological conditions. The method is also
XX CC useful for evaluating samples containing several analytes/biopolymers for
XX CC the presence of physiological condition specific sequences. The peptide
XX CC presented is a biomarker from alpha fibrinogen and is associated with
XX CC myocardial infarction (MI) and renal failure

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 65; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
| | | | | | | | | |
DB 2 SESDFLAEGGGVR 14

RESULT 3

ABG76138
ID ABG76138 standard; peptide; 15 AA.

XX AC ABG76138;

XX DT 08-MAY-2003 (first entry)

XX DE Human alpha fibrinogen peptide #1.

XX KW Human; alpha fibrinogen; renal failure; myocardial infarction;
XX KM unstable angina; matrix assisted laser desorption-time of flight;
XX KM MALDI-TOF; mass spectroscopy; antigen.

XX OS Homo sapiens.

XX PN US2002160528-A1.

XX PD 31-OCT-2002.

XX PF 30-APR-2001; 2001US-00845729.

XX PR 30-APR-2001; 2001US-00845729.

XX PA (JACK/) JACKOWSKI G.

XX PA (THAT/) THATCHER B.

XX PA (MARS/) MARSHALL J.

XX PA (YANT/) YANTHA J.

XX PA (VREE/) VREES T.

XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;

XX DR WPI; 2003-255194/25.

XX PT Novel biopolymer marker such as alpha fibrinogen having specific
XX PT molecular weight, useful in indicating disease state such as myocardial
XX PT infarction or renal failure.

XX PS Disclosure; Fig 1; 10pp; English.

XX CC The invention relates a biopolymer marker such as alpha fibrinogen having
XX CC a molecular weight of about 1350 daltons and a sequence appearing as
XX CC ABG76139 useful in indicating at least one particular disease state. The
XX CC presence of the peptide in a sample is determined by matrix assisted
XX CC laser desorption-time of flight (MALDI-TOF) mass spectroscopy. The marker
XX CC is useful for indicating at least one particular disease state such as
XX CC myocardial infarction or renal failure (e.g. in a patient presenting with
XX CC unstable angina). The biopolymer marker is useful as antigen in
XX CC immunoassays for the detection of those individuals suffering from the
XX CC disease known to be evidenced by the marker sequence. The biopolymer
XX CC marker rapidly and accurately diagnoses a disease state such as
XX CC myocardial infarction or renal failure, and allows physicians to identify
XX CC asymptomatic patients before they suffer from the disease state. The
XX CC present sequence is an alpha fibrinogen biopolymer marker

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 65; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
| | | | | | | | | |
DB 2 SESDFLAEGGGVR 14

RESULT 4
ABU09252
ID ABU09252 standard; peptide; 12 AA.
XX AC ABU09252;
XX DT 24-JUN-2003 (first entry)
XX DE Human alpha fibrinogen peptide.
XX KW Human; alpha fibrinogen; renal failure; Syndrome X; insulin resistance;
KW dyslipidaemia; hypertension; obesity; non-insulin dependent diabetes.
XX OS Homo sapiens.
XX PN US2002161185-A1.
XX PD 31-OCT-2002.
XX PF 30-APR-2001; 2001US-00845725.
XX PR 30-APR-2001; 2001US-00845725.
XX PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX WPI; 2003-370707/35.
XX DR WPI; 2003-370707/35.
XX PT Novel biopolymer marker useful for indicating a particular disease state,
PT e.g. renal failure, comprises a peptide sequence of 12 amino-acids.
XX PS Claim 1; Page 7; 10pp; English.
XX CC The invention relates to a biopolymer marker useful for indicating at
CC least one particular disease state e.g. renal failure. The biopolymer
CC marker is useful for developing diagnostic test to identify asymptomatic
CC patients before they suffer an irreversible event. The biopolymer marker
CC enables a diagnostician to gain the ability to characterise either the
CC presence or absence of the at least one disease state relative to the
CC recognition of the presence or absence of the biopolymer. The marker may
CC be of particular use in early diagnosis of Syndrome X, a multi-faceted
CC disease characterised by insulin resistance, dyslipidaemia, hypertension,
CC obesity and non-insulin dependent diabetes. The present sequence is the
CC biopolymer marker of the invention being a peptide derived from human
CC alpha fibrinogen
XX SQ Sequence 12 AA;
Query Match 87.7%; Score 57; DB 6; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0051;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ESDFLAEGGGVR 13
DB 1 EGDFLAEGGGVR 12
RESULT 5
ABU08825
ID ABU08825 standard; peptide; 13 AA.
XX AC ABU08825;
XX DT 25-AUG-2003 (first entry)
XX DE Alpha fibrinogen peptide, #2, used for myocardial infarction diagnostics.
XX KW Alpha fibrinogen; human; myocardial infarction; SELDI; mass spectrometry;
KW surfaces enhanced for laser desorption/ionisation.
XX OS Homo sapiens.
XX PN US2002160422-A1.
XX PD 31-OCT-2002.
XX PF 30-APR-2001; 2001US-00846342.
KW Proteomic; human; physiological condition; analyte; biopolymer;
KW biomarker; alpha fibrinogen; myocardial infarction; MI.
XX OS Homo sapiens.
XX PN US2002160420-A1.
XX PD 31-OCT-2002.
XX PF 30-APR-2001; 2001US-00846330.
XX PR 30-APR-2001; 2001US-00846330.
XX PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX WPI; 2003-491923/46.
XX DR WPI; 2003-491923/46.
XX PT Determining proteomic basis e.g. basis for diagnosing existence of or
PT predicting development and/or progression of abnormal physiological
PT conditions based upon the presence of proteomic materials.
XX PS Disclosure; Page 10; 25pp; English.
XX CC The invention discloses a method for determining a proteomic basis for
CC development and progression of abnormal physiological conditions. The
CC method comprises isolating one or more patient specific proteomic
CC materials from a sample and comparing it against a library of proteomic
CC materials having characteristics identifiable with both normal and
CC abnormal physiological conditions or their predictive hallmarks. The
CC method is useful for determining a proteomic basis for development and
CC progression of abnormal physiological conditions. The method is also
CC useful for evaluating samples containing several analytes/biopolymers for
CC the presence of physiological condition specific sequences. The peptide
CC presented is a biomarker from alpha fibrinogen and is associated with
CC myocardial infarction (MI)
XX SQ Sequence 13 AA;
Query Match 87.7%; Score 57; DB 6; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ESDFLAEGGGVR 13
DB 1 EGDFLAEGGGVR 12
RESULT 6
ADA18539
ID ADA18539 standard; peptide; 13 AA.
XX AC ADA18539;
XX DT 20-NOV-2003 (first entry)
XX DE Human alpha fibrinogen peptide #1.
XX KW Alpha fibrinogen; human; myocardial infarction; SELDI; mass spectrometry;
KW surfaces enhanced for laser desorption/ionisation.
XX OS Homo sapiens.
XX PN US2002160422-A1.
XX PD 31-OCT-2002.
XX PF 30-APR-2001; 2001US-00846342.

```

XX 30-APR-2001; 2001US-00846342.
XX (JACK/) JACKOWSKI G.
XX (THAT/) THATCHER B.
XX (MARS/) MARSHALL J.
XX (YANT/) YANTHA J.
XX (VREE/) VREES T.
XX Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX WPI; 2003-219986/21.
XX Novel biopolymer marker useful in indicating disease state, in particular
XX myocardial infarction.
XX Disclosure; Fig 1; 10pp; English.
XX The invention relates to a biopolymer marker useful in indicating at
XX least one particular disease state. This marker is characterised as alpha
XX fibrinogen having a molecular weight of 1077 Daltons and is useful for
XX indicating a disease state, in particular myocardial infarction. The
XX marker sequences are useful as antigens in immunoassays for the detection
XX of those individuals suffering from the disease known to be evidenced by
XX the marker sequence. The marker provides an efficient diagnostic tool for
XX rapidly and accurately diagnosing disease states such as myocardial
XX infarction. The marker was detected by the technique of surfaces enhanced
XX for laser desorption/ionisation (SELDI) mass spectroscopy. The present
XX sequence is the detected alpha fibrinogen marker peptide.
XX Sequence 13 AA;
XX
XX Query Match 87.7%; Score 57; DB 6; Length 13;
XX Best Local Similarity 91.7%; Pred. No. 0.0055;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 ESDFLAEGGGVR 13
XX | | | | | | | |
XX Db 1 EGDFLAEGGGVR 12
XX
XX RESULT 7
XX ABU08827
XX ID ABU08827 standard; peptide; 14 AA.
XX
XX AC ABU08827;
XX
XX 25-AUG-2003 (first entry)
XX
XX DE Alpha fibrinogen peptide, #3, used for renal failure diagnostics.
XX
XX KW Proteomic; human; physiological condition; analyte; biopolymer;
XX biomarker; alpha fibrinogen; renal failure.
XX
XX OS Homo sapiens.
XX
XX PN US2002160420-A1.
XX
XX PD 31-OCT-2002.
XX
XX 30-APR-2001; 2001US-00846330.
XX
XX 30-APR-2001; 2001US-00846330.
XX
XX (JACK/) JACKOWSKI G.
XX (THAT/) THATCHER B.
XX (MARS/) MARSHALL J.
XX (YANT/) YANTHA J.
XX (VREE/) VREES T.
XX Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX WPI; 2003-491923/46.
XX
XX 30-APR-2001; 2001US-00846342.
XX (JACK/) JACKOWSKI G.
XX (THAT/) THATCHER B.
XX (MARS/) MARSHALL J.
XX (YANT/) YANTHA J.
XX (VREE/) VREES T.
XX Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX WPI; 2003-219986/21.
XX Novel biopolymer marker useful in indicating disease state, in particular
XX myocardial infarction.
XX Disclosure; Fig 1; 10pp; English.
XX The invention relates to a biopolymer marker useful in indicating at
XX least one particular disease state. This marker is characterised as alpha
XX fibrinogen having a molecular weight of 1077 Daltons and is useful for
XX indicating a disease state, in particular myocardial infarction. The
XX marker sequences are useful as antigens in immunoassays for the detection
XX of those individuals suffering from the disease known to be evidenced by
XX the marker sequence. The marker provides an efficient diagnostic tool for
XX rapidly and accurately diagnosing disease states such as myocardial
XX infarction. The marker was detected by the technique of surfaces enhanced
XX for laser desorption/ionisation (SELDI) mass spectroscopy. The present
XX sequence is the detected alpha fibrinogen marker peptide.
XX Sequence 13 AA;
XX
XX Query Match 87.7%; Score 57; DB 6; Length 13;
XX Best Local Similarity 91.7%; Pred. No. 0.0055;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 ESDFLAEGGGVR 13
XX | | | | | | | |
XX Db 1 EGDFLAEGGGVR 12
XX
XX RESULT 8
XX AAR96194
XX ID AAR96194 standard; peptide; 16 AA.
XX
XX AC AAR96194;
XX
XX 19-DEC-1996 (first entry)
XX
XX DE Fibrinogen epitope probe, represents alpha chain residues 1-16.
XX
XX KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
XX monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
XX sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
XX pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
XX chronic obstructive pulmonary disease; myelogenous leukaemia;
XX infantile respiratory distress syndrome; gout;
XX adult respiratory distress syndrome.
XX
XX OS Homo sapiens.
XX
XX PN WO9614580-A1.
XX
XX PD 17-MAY-1996.
XX
XX PF 03-NOV-1995; 95WO-US013794.
XX
XX PR 07-NOV-1994; 94US-00335524.
XX 06-JUN-1995; 95US-00469141.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Mumford RA, Davies DTP, Dahlgren ME, Boger JS, Humes JL;
XX WPI; 1996-251888/25.
XX New isolated fibrinogen derived cleavage products - used for detection of
XX leukocyte elastase activity in disease diagnosis and for evaluating
XX elastase inhibitors.
XX Example 5; Page 42; 109pp; English.
XX The sequences given in AAR96182-94 represent antigenic probes derived

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Determining proteomic basis e.g. basis for diagnosing existence of or predicting development and/or progression of abnormal physiological conditions based upon the presence of proteomic materials.

Disclosure; Page 10; 25pp; English.

The invention discloses a method for determining a proteomic basis for development and progression of abnormal physiological conditions. The method comprises isolating one or more patient specific proteomic materials from a sample and comparing it against a library of proteomic materials having characteristics identifiable with both normal and abnormal physiological conditions or their predictive hallmarks. The method is useful for determining a proteomic basis for development and progression of abnormal physiological conditions. The method is also useful for evaluating samples containing several analyses/biopolymers for the presence of physiological condition specific sequences. The peptide presented is a biomarker from alpha fibrinogen and is associated with renal failure

Sequence 14 AA;

Query Match 87.7%; Score 57; DB 6; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.006;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13

Db 2 EGDFLAEGGGVR 13

RESULT 8

AAR96194

ID AAR96194 standard; peptide; 16 AA.

AC AAR96194;

DT 19-DEC-1996 (first entry)

DE Fibrinogen epitope probe, represents alpha chain residues 1-16.

KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen; monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid; sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis; pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis; chronic obstructive pulmonary disease; myelogenous leukaemia; infantile respiratory distress syndrome; gout; adult respiratory distress syndrome.

OS Homo sapiens.

PN WO9614580-A1.

PD 17-MAY-1996.

PF 03-NOV-1995; 95WO-US013794.

PR 07-NOV-1994; 94US-00335524.

06-JUN-1995; 95US-00469141.

(MERI) MERCK & CO INC.

Mumford RA, Davies DTP, Dahlgren ME, Boger JS, Humes JL;

WPI; 1996-251888/25.

New isolated fibrinogen derived cleavage products - used for detection of leukocyte elastase activity in disease diagnosis and for evaluating elastase inhibitors.

Example 5; Page 42; 109pp; English.

The sequences given in AAR96182-94 represent antigenic probes derived

from the first 21 amino acids of human fibrinogen. These probes are used to determine antibody titre against other fibrinogen cleavage products. The monospecific antibodies may be used to assay for the formation of complementary cleavage product antigens or epitopes in whole blood or other body fluids, peritoneal fluid, sputum or bronchoalveolar lavage fluid. The assay for cleavage products is dependent upon the presence of HLE in the sample. This assay can also be used for the evaluation of HLE inhibitors. The antibodies may be used to diagnose and monitor diseases such as arthritis, gout, pulmonary emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive pulmonary disease, bronchiectasis, adult or infantile respiratory distress syndrome and myelogenous leukaemia. See also AAR96146-81

Sequence 16 AA;

Query Match	87.7%	Score 57;	DB 2;	Length 16;
Best Local Similarity	91.7%	Pred. No. 0.0069;		
Matches 11;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

Qy 2 ESDFLAEGGGV 13
Db 5 EGDFLAEGGGV 16

RESULT 9
AAW04619
ID AAW04619 standard; peptide; 16 AA.

AAW04619;

DT 13-AUG-1997 (first entry)

Fibrinopeptide A pentide f

Mass spectrometer: polymer

XX 50 Synthetic

XX
DN W09636986-A1

XX 31 MAY 1966

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PR 19-MAY-1995; 95US-00447175.

PA (PERS-) PERCEPTIVE BIOSYSTEMS INC.

PI Patterson DH, Tarr GE;

DR WPI; 1997-012308/01.

Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins, etc.
 - by obtaining mass to charge ratios of polymer fragments, pref. using mass spectrometer, and performing statistical analysis.

PS Example 2; Page 32; 86pp; English.

A method of obtaining sequence information about a polymer (e.g. DNA, RNA, peptide nucleic acids, proteins, peptides and carbohydrates) comprising monomers of known mass has been claimed. The present sequence represents a fibrinopeptide A peptide, and was used as an example as a digestion before analysis by mass spectrometry, using this novel on-plate strategy. Total sequence information from a nine well digestion can be represented in a single digestion or it is often derived from two or more wells. The methods, apparatus and kit (claimed) can be used for the analysis of polymers, particularly biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides and carbohydrates. It provides a rapid, automated and cost effective sequencing of polymers, with a statistical certainty

Sequence 16 AA;

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%;
Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels

Qy	2	ESDFLAEGGGV	13
Db	5	EGDFLAEGGGV	16

RESULT 10

AA157487
ID AAY57487 standard; peptide; 16 AA.

AC AAY57487:

XX
DT 25-FEB-2000 (first entry)XX DE Antimicrobial peptide CS-FBP- α SE0 TN NO-25

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; KW
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. KW
XX

XX QS Synthetic

OS
yy
Cryptolagus c

PN WO9942119-A1.
yy

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US003350.

PR 18-FEB-1998; 98US-00025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI; 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

PS Disclosure: Page 120: 166pp: English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXBXBXB and its derivatives selected from XBZBXBXBXBXB, BXZXB, BXZGXZXB, XBZBXBXBXBX and BXZBXBXZ; and (b) a second peptide template XBEXBX and their derivatives selected from the group consisting of XBZBXBXB, XBZBXBXBX, BXZBXBXB, XBZBXBXB, and XBZBXBXBXZBXBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention

Sequence 16 AA:
XX
SO

Sequence 16 AA;

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels

Qy 2 ESDFLAEGGVR 13
Db 5 EGDFLAEGGVR 16

Db 5 EGDFLAEGGGVR 16

RESULT 11
 ABB56219 standard; peptide; 16 AA.
 ID ABB56219 standard; peptide; 16 AA.
 XX AC ABB56219;
 XX DT 15-FEB-2002 (first entry)
 XX DE Vascular dementia-associated protein isoform (VPI) 419.
 XX KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 XX KW diagnosis; prognosis; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200169261-A2.
 XX PD 20-SEP-2001.
 XX PF 14-MAR-2001; 2001WO-GB001106.
 XX PR 15-MAR-2000; 2000GB-00006285.
 XX PR 24-NOV-2000; 2000GB-00028734.
 XX PR 28-NOV-2000; 2000US-00724391.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMWAC, Parekh RB, Rohlf C;
 XX WPI; 2001-557937/62.
 XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy, for
 PT comprises analysing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX PS Claim 6; Page 39; 151pp; English.
 XX The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 23 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy
 XX SQ Sequence 16 AA;
 Query Match 87.7%; Score 57; DB 4; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.0069;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 Db | |||||
 5 EGDFLAEGGGVR 16
 RESULT 12
 AAB91959 standard; peptide; 16 AA.
 ID AAB91959
 XX AC AAB91959;
 XX DT 22-JUN-2001 (first entry)
 XX KW Fibronectin fragment and fibrin related peptide SEQ ID NO:1135.
 DE

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200069900-A2.
 XX PD 23-NOV-2000.
 XX PF 17-MAY-2000; 2000WO-US013576.
 XX PR 17-MAY-1999; 99US-0134406P.
 XX PR 10-SEP-1999; 99US-0153406P.
 XX PR 15-OCT-1999; 99US-0159783P.
 XX PA (CONJ-) CONJUCHEM INC.
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX WPI; 2001-112059/12.
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX PS Disclosure; Page 567; 733pp; English.
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX SQ Sequence 16 AA;
 Query Match 87.7%; Score 57; DB 4; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.0069;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 Db | |||||
 5 EGDFLAEGGGVR 16
 RESULT 13
 ABB52337 standard; peptide; 16 AA.
 ID ABB52337
 XX AC ABB52337;
 XX DT 08-FEB-2002 (first entry)
 XX DE Human API-118 tryptic digest peptide #2.
 XX KW Human; neuroprotective; nootropic; gene therapy; vaccine;
 KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
 KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
 KW Expression Reference Protein Isoform; ERPI; proteolysis.
 XX

OS Homo sapiens.
 PN WO200175454-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010908.
 XX
 PR 03-APR-2000; 2000US-0194504P.
 PR 28-NOV-2000; 2000US-0253647P.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA (PFIZ) PFIZER INC.
 XX
 PI Durham KI, Friedman DL, Herath HM, Kimmel LH, Parekh RB;
 PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
 PI Townsend RR, White F, Williams SA;
 XX WPI; 2001-639384/73.
 XX
 XX Screening for Alzheimer's disease in a mammal, by making two-dimensional
 PT array of a feature whose relative abundance correlates with disease, and
 PT comparing with abundance of the feature in samples of healthy persons.
 XX
 PS Example; Page 33; 162pp; English.
 XX
 XX The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection of
 CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
 CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
 CC plasma. The abundance of the AFs and APIs is then normalised to an
 CC Expression Reference Protein Isoform (BRPI) in order to determine whether
 CC a patient is suffering from, or has a predisposition to, Alzheimer's
 CC disease. The relative abundance of the AFs and APIs correlates with the
 CC severity of Alzheimer's disease. The present sequence is a peptide
 CC produced from an API by proteolysis
 XX
 SQ Sequence 16 AA;
 Query Match 87.7%; Score 57; DB 4; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.0069;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 Db | | | | | | | | | |
 5 EGDFLAEGGGVR 16
 RESULT 14
 ABG73668
 ID ABG73668 standard; peptide; 16 AA.
 AC ABG73668;
 XX
 DT 11-MAR-2003 (first entry)
 XX
 DE Linear HIV-1 gp120 V3-loop derived peptide ligand SEQ ID 11.
 XX
 KW gp120; interaction; co-receptor; CXCR4; CCR5; refractive index; V3 loop;
 KW 7-helix transmembrane receptor; glycopeptide; virucide; anti-HIV;
 KW HIV infection.
 XX
 OS Human immunodeficiency virus 1.
 OS Synthetic.
 XX
 PN DE10113042-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 09-MAR-2001; 2001DE-01013042.
 XX
 PR 09-MAR-2001; 2001DE-01013042.
 XX
 PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
 PT determining the stage or severity of MS, comprises detecting the presence

(NOCH-) NOCHT INST TROPENMEDIZIN BERNHARD.
 Schreiber M, Seifert A, Meyer B;
 WPI; 2002-752120/82.
 Identifying compounds that modify interaction of gp120 and co-receptors,
 useful potentially for treating human immune deficiency virus infection,
 also new peptides.
 Claim 10; Page 56; 68pp; German.
 This invention describes novel substances that modify the interaction
 between the gp120 protein of human immunodeficiency virus (HIV), or its
 fragments, with the co-receptors CXCR4, CCR5 and/or other 7-helix
 transmembrane receptors for HIV. The method comprises (a) immobilizing a
 ligand for the co-receptor on a gold surface; (b) contacting the ligand
 with suspended cells that express the co-receptor; and (c) determining
 interaction by measuring the refractive index (RI) by plasmon resonance.
 The procedure is repeated using cells that have been incubated with a
 test compound, and this is identified if RI is lower for cells
 preincubated with it. The ligand is a linear or cyclic (glyco)peptide
 that includes the amino acid sequence of an HIV V3 loop (including
 flanking Cys). The products of the invention have virucide and anti-HIV
 (human immunodeficiency virus) activity and are useful for prevention
 and/or treatment of HIV infection. This sequence represents a linear HIV
 1 gp120 V3-loop derived peptide ligand described in the disclosure of the
 invention
 Sequence 16 AA;
 Query Match 87.7%; Score 57; DB 5; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.0069;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 Db | | | | | | | | | |
 5 EGDFLAEGGGVR 16
 RESULT 15
 ABG78799
 ID ABG78799 standard; peptide; 16 AA.
 AC ABG78799;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #287.
 KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSF;
 KW human; multiple sclerosis-associated protein isoform; MSPI;
 KW antiinflammatory; neuroprotective.
 XX
 OS Homo sapiens.
 OS
 PN WO200259604-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 25-JAN-2002; 2002WO-GB000330.
 PR 26-JAN-2001; 2001US-0264404P.
 PR 20-NOV-2001; 2001US-0331647P.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herath HM, Parekh RB, Rohlf C;
 XX
 WPI; 2002-599812/64.
 Screening or diagnosing multiple sclerosis (MS), useful for e.g.
 determining the stage or severity of MS, comprises detecting the presence

PT of MS-associated features or protein isoforms by 2-dimensional
FT electrophoresis.

PS Disclosure; Page 32; 128pp; English.

XX This invention relates to a novel method for screening or diagnosing
CC multiple sclerosis (MS) in a subject to determine the stage or severity
CC of MS, to identify a subject at risk of developing MS or to monitor the
CC effect of a therapy administered. The method comprises analysing a sample
CC body fluid from the subject by two-dimensional electrophoresis and
CC detecting the presence of multiple sclerosis-associated features (MSFs),
CC or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of
CC the invention correspond to spots identified on a 2D gel these proteins
CC may have antiinflammatory or neuroprotective activity. The methods of the
CC invention and the compositions are useful for clinical screening,
CC diagnosis and treatment of MS, for monitoring the effectiveness of MS
CC treatments, for selecting participants in clinical trials, for identifying
CC patients most likely to respond to a particular therapeutic treatment and
CC for screening and developing drugs for treatment of MS. Agents that
CC modulate the expression or activity of an MSPI are useful for treating
CC MS, for preventing or delaying the onset or development of MS, to prevent
CC or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic
CC acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,
CC or their fragments are useful for promoting MSPI function by gene
CC therapy. The present sequence represents a human multiple sclerosis
CC associated feature tryptic digest peptide of the invention

XX SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 5; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.0069;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13

Db 5 EGDFLAEGGGVR 16

Search completed: April 27, 2004, 16:23:58
Job time : 56 secs